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1600

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/380,015BDATE: 06/06/2002
TIME: 15:18:13Input Set : A:\sequence.txt
Output Set: N:\CRF3\06062002\I380015B.raw

ENTERED

SEQUENCE LISTING

4 (1) GENERAL INFORMATION:

6 (i) APPLICANT: Carsten Korth

8 (ii) TITLE OF INVENTION: Immunological Detection of Prions

10 (iii) NUMBER OF SEQUENCES: 9

12 (iv) CORRESPONDENCE ADDRESS:

13 (A) ADDRESSEE: Kanton Zuerich vertreten durch die Erziehungsdirektion

14 (B) STREET: Walchetur

15 (C) CITY: Zuerich

16 (D) STATE: Zuerich

17 (E) COUNTRY: Switzerland

18 (F) ZIP: CH-8090

20 (v) COMPUTER READABLE FORM:

21 (A) MEDIUM TYPE: Floppy disk

22 (B) COMPUTER: IBM PC compatible

23 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

24 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

26 (vi) CURRENT APPLICATION DATA:

27 (A) APPLICATION NUMBER: US/09/380,015B

28 (B) FILING DATE: 23-Aug-1999

30 (vii) PRIOR APPLICATION DATA:

31 (A) APPLICATION NUMBER: EP 97102837.8

32 (B) FILING DATE: 21-FEB-1997

35 (2) INFORMATION FOR SEQ ID NO: 1:

37 (i) SEQUENCE CHARACTERISTICS:

38 (A) LENGTH: 660 base pairs

39 (B) TYPE: nucleic acid

40 (C) STRANDEDNESS: double

41 (D) TOPOLOGY: linear

43 (ii) MOLECULE TYPE: DNA (genomic)

45 (iii) HYPOTHETICAL: NO

47 (iv) ANTI-SENSE: NO

49 (vi) ORIGINAL SOURCE:

50 (A) ORGANISM: Bos taurus

51 (D) DEVELOPMENTAL STAGE: Adult

53 (vii) IMMEDIATE SOURCE:

54 (B) CLONE: pbPrP3

58 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

60 ATGAAGAACG GACAAAACC TGGAGGAGGA TGGAACACTG GGGGGAGCCG ATACCCAGGA	60
62 CAGGGCAGTC CTGGAGGCAA CCGTTATCCA CCTCAGGGAG GGGGTGGCTG GGGTCAGCCC	120
64 CATGGAGGTC GCTGGGGCCA GCCTCATGGA GGTGGCTGGG GCCAGCCTCA TGGAGGTGGC	180
66 TGGGGTCAGC CCCATGGTGG TGGCTGGGA CAGCCACATG GTGGTGGAGG CTGGGGTCAA	240
68 GGTGGTACCC ACGGTCAATG GAACAAACCC AGTAAGCCAA AAACCAACAT GAAGCATGTG	300

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70	GCAGGAGCTG	CTGCAGCTGG	AGCAGTGGTA	GGGGGCCCTTG	GTGGCTACAT	GCTGGGAAGT	360
72	GCCATGAGCA	GGCCTCTTAT	ACATTTGGC	AGTGAATATG	AGGACCGTTA	CTATCGTCAA	420
74	AACATGCACC	GTTACCCCAA	CCAAGTGTAC	TACAGGCCAG	TGGATCAGTA	TAGTAACCAG	480
76	ACAAACTTTC	TGCATGACTG	TGTCAACATC	ACAGTCAAGG	AACACACAGT	CACCAACCACC	540
78	ACCAAGGGGG	AGAACTTCAC	CGAAACTGAC	ATCAAGATGA	TGGAGCGAGT	GGTGGAGCAA	600
80	ATGTGCATTA	CCCAGTACCA	GAGAGAATCC	CAGGCTTATT	ACCAACGAGG	GGCAAGTTAA	660

83 (2) INFORMATION FOR SEQ ID NO: 2:

85 (i) SEQUENCE CHARACTERISTICS:
86 (A) LENGTH: 219 amino acids
87 (B) TYPE: amino acid
88 (C) STRANDEDNESS: single
89 (D) TOPOLOGY: linear
91 (ii) MOLECULE TYPE: protein
93 (iii) HYPOTHETICAL: YES
95 (iv) ANTI-SENSE: NO
97 (vi) ORIGINAL SOURCE:
98 (A) ORGANISM: Bos taurus

101 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
103 Met Lys Lys Arg Pro Lys Pro Gly Gly Gly Trp Asn Thr Gly Gly Ser
104 1 5 10 15
106 Arg Tyr Pro Gly Gln Gly Ser Pro Gly Gly Asn Arg Tyr Pro Pro Gln
107 20 25 30
109 Gly Gly Gly Trp Gly Gln Pro His Gly Gly Gly Trp Gly Gln Pro
110 35 40 45
112 His Gly Gly Trp Gly Gln Pro His Gly Gly Gly Trp Gly Gln Pro
113 50 55 60
115 His Gly Gly Trp Gly Gln Pro His Gly Gly Gly Trp Gly Gln
116 65 70 75 80
118 Gly Gly Thr His Gly Gln Trp Asn Lys Pro Ser Lys Pro Lys Thr Asn
119 85 90 95
121 Met Lys His Val Ala Gly Ala Ala Ala Gly Ala Val Val Gly Gly
122 100 105 110
124 Leu Gly Gly Tyr Met Leu Gly Ser Ala Met Ser Arg Pro Leu Ile His
125 115 120 125
127 Phe Gly Ser Asp Tyr Glu Asp Arg Tyr Tyr Arg Glu Asn Met His Arg
128 130 135 140
130 Tyr Pro Asn Gln Val Tyr Tyr Arg Pro Val Asp Gln Tyr Ser Asn Gln
131 145 150 155 160
133 Asn Asn Phe Val His Asp Cys Val Asn Ile Thr Val Lys Glu His Thr
134 165 170 175
136 Val Thr Thr Thr Lys Gly Glu Asn Phe Thr Glu Thr Asp Ile Lys
137 180 185 190
139 Met Met Glu Arg Val Val Glu Gln Met Cys Ile Thr Gln Tyr Gln Arg
140 195 200 205
142 Glu Ser Gln Ala Tyr Tyr Gln Arg Gly Ala Ser
143 210 215
145 (2) INFORMATION FOR SEQ ID NO: 3:
147 (i) SEQUENCE CHARACTERISTICS:
148 (A) LENGTH: 33 base pairs

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149 (B) TYPE: nucleic acid
150 (C) STRANDEDNESS: single
151 (D) TOPOLOGY: linear
153 (ii) MOLECULE TYPE: other nucleic acid
154 (A) DESCRIPTION: /desc = "oligonucleotide"
156 (iii) HYPOTHETICAL: NO
158 (iv) ANTI-SENSE: NO
163 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
165 GGGATTCCA TATGAAGAAG CGACCAAAAC CTG 33
167 (2) INFORMATION FOR SEQ ID NO: 4:
169 (i) SEQUENCE CHARACTERISTICS:
170 (A) LENGTH: 31 base pairs
171 (B) TYPE: nucleic acid
172 (C) STRANDEDNESS: single
173 (D) TOPOLOGY: linear
175 (ii) MOLECULE TYPE: other nucleic acid
176 (A) DESCRIPTION: /desc = "oligonucleotide"
178 (iii) HYPOTHETICAL: NO
180 (iv) ANTI-SENSE: NO
183 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
185 CGGGATCCTA TTAACATTGCC CCTCGTTGGT A 31
187 (2) INFORMATION FOR SEQ ID NO: 5:
189 (i) SEQUENCE CHARACTERISTICS:
190 (A) LENGTH: 5 amino acids
191 (B) TYPE: amino acid
192 (C) STRANDEDNESS: single
193 (D) TOPOLOGY: linear
195 (ii) MOLECULE TYPE: peptide
197 (iii) HYPOTHETICAL: YES
199 (iv) ANTI-SENSE: NO
204 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
206 Leu Ile His Phe Gly
207 1 5
209 (2) INFORMATION FOR SEQ ID NO: 6:
211 (i) SEQUENCE CHARACTERISTICS:
212 (A) LENGTH: 9 amino acids
213 (B) TYPE: amino acid
214 (C) STRANDEDNESS: single
215 (D) TOPOLOGY: linear
217 (ii) MOLECULE TYPE: peptide
219 (iii) HYPOTHETICAL: YES
221 (iv) ANTI-SENSE: NO
226 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
228 Asp Tyr Glu Asp Arg Tyr Tyr Arg Glu
229 1 5
231 (2) INFORMATION FOR SEQ ID NO: 7:
233 (i) SEQUENCE CHARACTERISTICS:
234 (A) LENGTH: 7 amino acids
235 (B) TYPE: amino acid

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236 (C) STRANDEDNESS: single
237 (D) TOPOLOGY: linear
239 (ii) MOLECULE TYPE: peptide
241 (iii) HYPOTHETICAL: YES
243 (iv) ANTI-SENSE: NO
248 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
250 Gly Ser Asp Tyr Glu Asp Arg
251 1 5
253 (2) INFORMATION FOR SEQ ID NO: 8:
255 (i) SEQUENCE CHARACTERISTICS:
256 (A) LENGTH: 9 amino acids
257 (B) TYPE: amino acid
258 (C) STRANDEDNESS: single
259 (D) TOPOLOGY: linear
261 (ii) MOLECULE TYPE: peptide
263 (iii) HYPOTHETICAL: YES
265 (iv) ANTI-SENSE: NO
270 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
272 Tyr Tyr Arg Pro Val Asp Gln Tyr Ser
273 1 5
275 (2) INFORMATION FOR SEQ ID NO: 9:
277 (i) SEQUENCE CHARACTERISTICS:
278 (A) LENGTH: 13 amino acids
279 (B) TYPE: amino acid
280 (C) STRANDEDNESS: single
281 (D) TOPOLOGY: linear
283 (ii) MOLECULE TYPE: peptide
285 (iii) HYPOTHETICAL: YES
287 (iv) ANTI-SENSE: NO
292 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:
294 Cys Ile Thr Gln Tyr Gln Arg Glu Ser Gln Ala Tyr Tyr
295 1 5 10

VERIFICATION SUMMARY
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L:27 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:28 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]